



results of BLAST

BLASTN 2.2.13 [Nov-27-2005]

RID: 1136323436-15309-195782079919.BLASTQ4

Database: ref_contig

3315 sequences; 2,411,399,953 total letters

If you have any problems or questions with the results of this search please refer to the [BLAST FAQs](#)

[Taxonomy reports](#)

Genome View

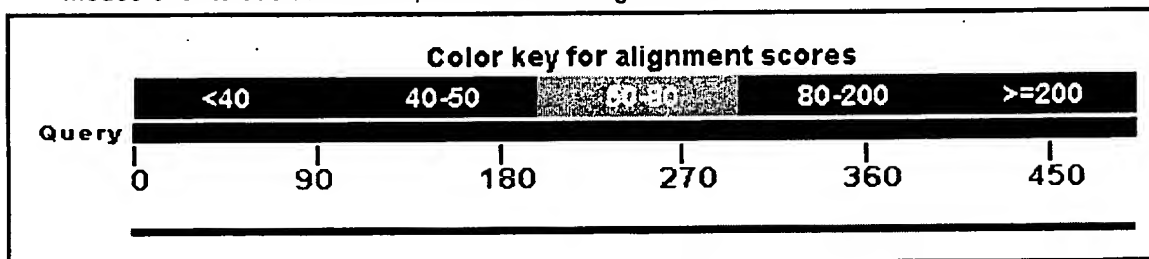
Show positions of the BLAST hits in the dog genome using the Entrez Genomes MapViewer

Query=

(492 letters)

Distribution of 1 Blast Hits on the Query Sequence

Mouse over to see the define, click to show alignments



Sequences producing significant alignments:

Score (Bits) E Value

ref|NW_879562.1|CfaX_WGA86_2 Canis familiaris chromosome X genom 912 0.0

Alignments

>ref|NW_879562.1|CfaX_WGA86_2 **D** Canis familiaris chromosome X genomic contig
Length=48572774

Features in this part of subject sequence:

similar to Rho-GTPase-activating protein 6 (Rho-type GTPa...

Score = 912 bits (474), Expect = 0.0

Identities = 492/492 (100%), Gaps = 0/492 (0%)

Strand=Plus/Plus

```

Query 1      ATGGGGACCTGGATTTTGTTCCTGCCTCCTGGGAGCAGCCTTTGCTATGCCCGTGAGT 60
            |||
Sbjct 7684216 ATGGGGACCTGGATTTTGTTCCTGCCTCCTGGGAGCAGCCTTTGCTATGCCCGTGAGT 768427

Query 61     AAAATACCCCTGCATAATATTCAATTTTACAAGCTTGGAAATAAAAGTCTGCCCCACAGT 120
            |||
Sbjct 7684276 AAAATACCCCTGCATAATATTCAATTTTACAAGCTTGGAAATAAAAGTCTGCCCCACAGT 768433

Query 121    TGGTAAACTTTAGGGTTTAAAGACAGTACAAGATCAGATGTCCTCAAATGTCTCTGTGTTT 180
            |||
Sbjct 7684336 TGGTAAACTTTAGGGTTTAAAGACAGTACAAGATCAGATGTCCTCAAATGTCTCTGTGTTT 768439

Query 181    AAGAAACACTTGGAAGAGCTTGTTATnnnnnnnnnnTATATTCCTCAGATGCCTCCACCCAA 240
            |||
Sbjct 7684396 AAGAAACACTTGGAAGAGCTTGTTATAAAAAATATATTCCTCAGATGCCTCCACCCAA 768445

Query 241    GACTGATTTCAGTAGAGCAGGAGTGGGGGGAGTGGCCAGGACTCTGCATTTTAACAAGCAC 300
            |||
Sbjct 7684456 GACTGATTTCAGTAGAGCAGGAGTGGGGGGAGTGGCCAGGACTCTGCATTTTAACAAGCAC 768451

Query 301    CTCAGGAGATTCTGTGGAGACAATTAACCTTGTAATATCATCGCCCATCTCTAGATGGAG 360
            |||
Sbjct 7684516 CTCAGGAGATTCTGTGGAGACAATTAACCTTGTAATATCATCGCCCATCTCTAGATGGAG 768457

Query 361    GAAACTTTTAGAAGGGACCCCTTGAAAGGCCTCCAGAGAAAGTGCTCGAACAGCTTAGGCA 420
            |||
Sbjct 7684576 GAAACTTTTAGAAGGGACCCCTTGAAAGGCCTCCAGAGAAAGTGCTCGAACAGCTTAGGCA 768463

Query 421    AATACTACAAAAATGCCAATTTTCTCTAAAACCCAATTTCTAACGAGTGTCCAACCTCTCT 480
            |||
Sbjct 7684636 AATACTACAAAAATGCCAATTTTCTCTAAAACCCAATTTCTAACGAGTGTCCAACCTCTCT 768469

Query 481    TCCTGCCCTCCA 492
            |||
Sbjct 7684696 TCCTGCCCTCCA 7684707

```

Database: dog build 2 genome database (reference assembly only)

Posted date: Sep 2, 2005 10:11 AM

Number of letters in database: -1,883,567,339

Number of sequences in database: 3,315

```

Lambda      K      H
1.33      0.621      1.12

```

Gapped

```

Lambda      K      H
1.33      0.621      1.12

```

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 3315

Number of Hits to DB: 3489

Number of extensions: 0

Number of successful extensions: 0

Number of sequences better than 0.01: 0

Number of HSP's better than 0.01 without gapping: 0

Number of HSP's gapped: 0

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Number of HSP's successfully gapped: 0
Number of extra gapped extensions for HSPs above 0.01: 0
Length of query: 492
Length of database: 2411399953
Length adjustment: 29
Effective length of query: 463
Effective length of database: 2411303818
Effective search space: 1116433667734
Effective search space used: 1116433667734
A: 0
X1: 18 (34.6 bits)
X2: 32 (59.1 bits)
X3: 27 (49.9 bits)
S1: 18 (34.4 bits)
S2: 25 (47.3 bits)